

SEQUENCE LISTING

<110> Bristol-Myers Squibb Company

<120> POLYNUCLEOTIDE ENCODING TWO NOVEL HUMAN POTASSIUM CHANNEL BETA-SUBUNITS,
K+betaM4 and K+betaM5

<130> D0115NP

<150> US 60/272,190

<151> 2001-02-28

<150> US 60/274,258

<151> 2001-03-07

<160> 98

<170> PatentIn version 3.0

<210> 1

<211> 1839

<212> DNA

<213> homo sapiens

<220>

<221> CDS

<222> (5)..(1057)

<400> 1

acaa atg acc ggg agc cat gac gtc atc ggg ggc gca gga aag cag gtg	49
Met Thr Gly Ser His Asp Val Ile Gly Gly Ala Gly Lys Gln Val	
1 5 10 15	

ctc tgc tgc ttt tgc aag cag aga aat aag agt ttg ggc acc tac cca	97
Leu Cys Cys Phe Cys Lys Gln Arg Asn Lys Ser Leu Gly Thr Tyr Pro	
20 25 30	

ggg gtc cca ggg aat gcc ctg tgg ctc ctg acc tcc ccc gcc tgt aat	145
Gly Val Pro Gly Asn Ala Leu Trp Leu Leu Thr Ser Pro Ala Cys Asn	
35 40 45	

gct ctg agc act tca gca gta atg cat gga aga gat aag ggg tct gtg	193
Ala Leu Ser Thr Ser Ala Val Met His Gly Arg Asp Lys Gly Ser Val	
50 55 60	

acc cat gga act gtc caa gtc ctc tct gac acc cgc ttc ttt tcc tgc	241
Thr His Gly Thr Val Gln Val Leu Ser Asp Thr Arg Phe Phe Ser Cys	
65 70 75	

cgt gaa gga cta ctt cca gca acc cag tct cct gcc atg tcc gac ccc	289
Arg Glu Gly Leu Leu Pro Ala Thr Gln Ser Pro Ala Met Ser Asp Pro	
80 85 90 95	

atc acg ctg aac gtc ggg ggg aag ctc tat aca acc tca ctg gcg acc	337
Ile Thr Leu Asn Val Gly Gly Lys Leu Tyr Thr Thr Ser Leu Ala Thr	
100 105 110	

ctg acc agc ttc cct gac tcc atg cta ggc gcc atg ttc agc ggg aag	385
Leu Thr Ser Phe Pro Asp Ser Met Leu Gly Ala Met Phe Ser Gly Lys	
115 120 125	
atg ccc acc aag agg gac agc cag ggc aac tgc ttc att gac cgt gac	433
Met Pro Thr Lys Arg Asp Ser Gln Gly Asn Cys Phe Ile Asp Arg Asp	
130 135 140	
ggc aaa gtg ttc cgc tat atc ctc aac ttc ctg cgg acc tcc cac ctt	481
Gly Lys Val Phe Arg Tyr Ile Leu Asn Phe Leu Arg Thr Ser His Leu	
145 150 155	
gac ctg cct gag gac ttc cag gag atg ggg ctg ctc cgc agg gag gcc	529
Asp Leu Pro Glu Asp Phe Gln Glu Met Gly Leu Leu Arg Arg Glu Ala	
160 165 170 175	
gac ttc tac cag gtg cag ccc ctg att gag gcc ctg cag gag aag gaa	577
Asp Phe Tyr Gln Val Gln Pro Leu Ile Glu Ala Leu Gln Glu Lys Glu	
180 185 190	
gtg gag ctc tcc aag gcc gag aag aat gcc atg ctc aac atc aca ctg	625
Val Glu Leu Ser Lys Ala Glu Lys Asn Ala Met Leu Asn Ile Thr Leu	
195 200 205	
aac cag cgt gtg cag acg gtc cac ttc act gtg cgc gag gca ccc cag	673
Asn Gln Arg Val Gln Thr Val His Phe Thr Val Arg Glu Ala Pro Gln	
210 215 220	
atc tac agc ctc tcc tct tcc agc atg gag gtc ttc aac gcc aac atc	721
Ile Tyr Ser Leu Ser Ser Ser Ser Met Glu Val Phe Asn Ala Asn Ile	
225 230 235	
ttc agc acc tcc tgc ctc ttc ctc aag ctc ctt ggc tct aag ctc ttc	769
Phe Ser Thr Ser Cys Leu Phe Leu Lys Leu Leu Gly Ser Lys Leu Phe	
240 245 250 255	
tac tgc tcc aat ggc aat ctc tcc tcc atc acc agc cac ttg cag gac	817
Tyr Cys Ser Asn Gly Asn Leu Ser Ser Ile Thr Ser His Leu Gln Asp	
260 265 270	
ccc aac cac ctg act ctg gac tgg gtg gcc aat gtg gag ggc ctg cca	865
Pro Asn His Leu Thr Leu Asp Trp Val Ala Asn Val Glu Gly Leu Pro	
275 280 285	
gag gag gag tac acc aag cag aac ctc aag agg ctc tgg gtg gtg ccc	913
Glu Glu Glu Tyr Thr Lys Gln Asn Leu Lys Arg Leu Trp Val Val Pro	
290 295 300	
gcc aac aag cag atc aac agc ttc cag gtc ttc gtg gaa gag gta ctg	961
Ala Asn Lys Gln Ile Asn Ser Phe Gln Val Phe Val Glu Glu Val Leu	
305 310 315	
aaa atc gct ctg agc gat ggc ttc tgc atc gat tct tct cac cca cat	1009
Lys Ile Ala Leu Ser Asp Gly Phe Cys Ile Asp Ser Ser His Pro His	
320 325 330 335	
gct ctg gat ttt atg aac aat aag att att cga tta ata cgg tac agg	1057

Ala Leu Asp Phe Met Asn Asn Lys Ile Ile Arg Leu Ile Arg Tyr Arg
340 345 350

taaaaggacc ccaacaacac tggagatggg gagtcccagg aagctcatgt cagccaggtc 1117
ttggagggca tctcgccagt ggtgcgaggc aggggactat actaatctgt attaattgtg 1177
tagcaggact tgattccccc catgatgaag tccacctttt ggaatccagt gtcctctgaa 1237
cagaaccacc ttttttcttg ccattttgag ctgcagacag gcggtttatt atgacaagtg 1297
aagagtcagc tgatgtgtac taaaggaggc cataggagga ttttccagcc aggacaaaag 1357
agcagcagtt ttctcctggg ctccatctct ctgtaccgct agccagtgcc gcatttatcc 1417
atctgtaaga aggccctggg ggagaggatg ggatgagaac aagaggctac ctccagttaa 1477
ccaggacata aagtccccag cggttcctgt cacacctgct cctccctccc cagggtgcat 1537
ccatgatcgt ggatgtttgc ccaggggtga ccatgtttgg ctggcttgga atgctgtgca 1597
ttctcagagc tctgttagtg tcccctcttg ggggtcagag atgaggtgtg gcaggggtcta 1657
gaggaatgag tgtccaggca gagttcagaa ggtaggaatg tccctcttga tagggctgaa 1717
tcaagggatt cctggcttta gaaaggggtct gctatctttg caaaaatgtg caagtatctg 1777
tagccagtgt aatgaaatca cttccaaatc caaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1837
aa 1839

<210> 2
<211> 351
<212> PRT
<213> homo sapiens

<400> 2

Met Thr Gly Ser His Asp Val Ile Gly Gly Ala Gly Lys Gln Val Leu
1 5 10 15

Cys Cys Phe Cys Lys Gln Arg Asn Lys Ser Leu Gly Thr Tyr Pro Gly
20 25 30

Val Pro Gly Asn Ala Leu Trp Leu Leu Thr Ser Pro Ala Cys Asn Ala
35 40 45

Leu Ser Thr Ser Ala Val Met His Gly Arg Asp Lys Gly Ser Val Thr
50 55 60

His Gly Thr Val Gln Val Leu Ser Asp Thr Arg Phe Phe Ser Cys Arg
65 70 75 80

Glu Gly Leu Leu Pro Ala Thr Gln Ser Pro Ala Met Ser Asp Pro Ile
 85 90 95

Thr Leu Asn Val Gly Gly Lys Leu Tyr Thr Thr Ser Leu Ala Thr Leu
 100 105 110

Thr Ser Phe Pro Asp Ser Met Leu Gly Ala Met Phe Ser Gly Lys Met
 115 120 125

Pro Thr Lys Arg Asp Ser Gln Gly Asn Cys Phe Ile Asp Arg Asp Gly
 130 135 140

Lys Val Phe Arg Tyr Ile Leu Asn Phe Leu Arg Thr Ser His Leu Asp
 145 150 155 160

Leu Pro Glu Asp Phe Gln Glu Met Gly Leu Leu Arg Arg Glu Ala Asp
 165 170 175

Phe Tyr Gln Val Gln Pro Leu Ile Glu Ala Leu Gln Glu Lys Glu Val
 180 185 190

Glu Leu Ser Lys Ala Glu Lys Asn Ala Met Leu Asn Ile Thr Leu Asn
 195 200 205

Gln Arg Val Gln Thr Val His Phe Thr Val Arg Glu Ala Pro Gln Ile
 210 215 220

Tyr Ser Leu Ser Ser Ser Ser Met Glu Val Phe Asn Ala Asn Ile Phe
 225 230 235 240

Ser Thr Ser Cys Leu Phe Leu Lys Leu Leu Gly Ser Lys Leu Phe Tyr
 245 250 255

Cys Ser Asn Gly Asn Leu Ser Ser Ile Thr Ser His Leu Gln Asp Pro
 260 265 270

Asn His Leu Thr Leu Asp Trp Val Ala Asn Val Glu Gly Leu Pro Glu
 275 280 285

Glu Glu Tyr Thr Lys Gln Asn Leu Lys Arg Leu Trp Val Val Pro Ala
 290 295 300

Asn Lys Gln Ile Asn Ser Phe Gln Val Phe Val Glu Glu Val Leu Lys
 305 310 315 320

Ile Ala Leu Ser Asp Gly Phe Cys Ile Asp Ser Ser His Pro His Ala
 325 330 335

Leu Asp Phe Met Asn Asn Lys Ile Ile Arg Leu Ile Arg Tyr Arg
 340 345 350

<210> 3
 <211> 237
 <212> PRT
 <213> homo sapiens

<400> 3

Met Asp Asn Gly Asp Trp Gly Tyr Met Met Thr Asp Pro Val Thr Leu
 1 5 10 15

Asn Val Gly Gly His Leu Tyr Thr Thr Ser Leu Thr Thr Leu Thr Arg
 20 25 30

Tyr Pro Asp Ser Met Leu Gly Ala Met Phe Gly Gly Asp Phe Pro Thr
 35 40 45

Ala Arg Asp Pro Gln Gly Asn Tyr Phe Ile Asp Arg Asp Gly Pro Leu
 50 55 60

Phe Arg Tyr Val Leu Asn Phe Leu Arg Thr Ser Glu Leu Thr Leu Pro
 65 70 75 80

Leu Asp Phe Lys Glu Phe Asp Leu Leu Arg Lys Glu Ala Asp Phe Tyr
 85 90 95

Gln Ile Glu Pro Leu Ile Gln Cys Leu Asn Asp Pro Lys Pro Leu Tyr
 100 105 110

Pro Met Asp Thr Phe Glu Glu Val Val Glu Leu Ser Ser Thr Arg Lys
 115 120 125

Leu Ser Lys Tyr Ser Asn Pro Val Ala Val Ile Ile Thr Gln Leu Thr
 130 135 140

Ile Thr Thr Lys Val His Ser Leu Leu Glu Gly Ile Ser Asn Tyr Phe
 145 150 155 160

Thr Lys Trp Asn Lys His Met Met Asp Thr Arg Asp Cys Gln Val Ser
 165 170 175

Phe Thr Phe Gly Pro Cys Asp Tyr His Gln Glu Val Ser Leu Arg Val
 180 185 190

~~His Leu Met Glu Tyr Ile Thr Lys Gln Gly Phe Thr Ile Arg Asn Thr~~

195					200					205									
Arg	Val	His	His	Met	Ser	Glu	Arg	Ala	Asn	Glu	Asn	Thr	Val	Glu	His				
					210					215					220				

Asn Trp Thr Phe Cys Arg Leu Ala Arg Lys Thr Asp Asp
225 230 235

```
<210> 4
<211> 256
<212> PRT
<213> homo sapiens

<220>
<221> UNSURE
<222> (15)..(15)
<223> wherein "X" is equal to any amino acid.
```

<400> 4

Met 1	Ser	Arg	Pro	Leu 5	Ile	Thr	Arg	Ser	Pro 10	Ala	Ser	Pro	Leu	Xaa 15	Asn
Gln	Gly	Ile	Pro 20	Thr	Pro	Ala	Gln	Leu 25	Thr	Lys	Ser	Asn	Ala 30	Pro	Val
His	Ile	Asp 35	Val	Gly	Gly	His	Met 40	Tyr	Thr	Ser	Ser	Leu 45	Ala	Thr	Leu
Thr	Lys 50	Tyr	Pro	Glu	Ser	Arg 55	Ile	Gly	Arg	Leu	Phe 60	Asp	Gly	Thr	Glu
Pro 65	Ile	Val	Leu	Asp 70	Ser	Leu	Lys	Gln	His 75	Tyr	Phe	Ile	Asp	Arg	Asp 80
Gly	Gln	Met	Phe	Arg 85	Tyr	Ile	Leu	Asn 90	Phe	Leu	Arg	Thr	Ser	Lys 95	Leu
Leu	Ile	Pro	Asp 100	Asp	Phe	Lys	Asp	Tyr 105	Thr	Leu	Leu	Tyr	Glu 110	Glu	Ala
Lys	Tyr	Phe 115	Gln	Leu	Gln	Pro	Met 120	Leu	Leu	Glu	Met	Glu 125	Arg	Trp	Lys
Gln	Asp 130	Arg	Glu	Thr	Gly	Arg 135	Phe	Ser	Arg	Pro	Cys 140	Glu	Cys	Leu	Val
Val 145	Arg	Val	Ala	Pro	Asp 150	Leu	Gly	Glu	Arg	Ile 155	Thr	Leu	Ser	Gly	Asp 160
Lys	Ser	Leu	Ile	Glu 165	Glu	Val	Phe	Pro	Glu 170	Ile	Gly	Asp	Val	Met 175	Cys
Asn	Ser	Val	Asn 180	Ala	Gly	Trp	Asn 185	His	Asp	Ser	Thr	His 190	Val	Ile	Arg

Phe Pro Leu Asn Gly Tyr Cys His Leu Asn Ser Val Gln Val Leu Glu
195 200 205

Arg Leu Gln Gln Arg Gly Phe Glu Ile Val Gly Ser Cys Gly Gly Gly
210 215 220

Val Asp Ser Ser Gln Phe Ser Glu Tyr Val Leu Arg Arg Glu Leu Arg
225 230 235 240

Arg Thr Pro Arg Val Pro Ser Val Ile Arg Ile Lys Gln Glu Pro Leu
245 250 255

<210> 5

<211> 234

<212> PRT

<213> homo sapiens

<400> 5

Met Pro His Arg Lys Glu Arg Pro Ser Gly Ser Ser Leu His Thr His
1 5 10 15

Gly Ser Thr Gly Thr Ala Glu Gly Gly Asn Met Ser Arg Leu Ser Leu
20 25 30

Thr Arg Ser Pro Val Ser Pro Leu Ala Ala Gln Gly Ile Pro Leu Pro
35 40 45

Ala Gln Leu Thr Lys Ser Asn Ala Pro Val His Ile Asp Val Gly Ser
50 55 60

His Met Tyr Thr Ser Ser Leu Ala Thr Leu Thr Lys Tyr Pro Asp Ser
65 70 75 80

Arg Ile Ser Arg Leu Phe Asn Gly Thr Glu Pro Ile Val Leu Asp Ser
85 90 95

Leu Lys Gln His Tyr Phe Ile Asp Arg Asp Gly Glu Ile Phe Arg Tyr
100 105 110

Val Leu Ser Phe Leu Arg Thr Ser Lys Leu Leu Leu Pro Asp Asp Phe
115 120 125

Lys Asp Phe Ser Leu Leu Tyr Glu Glu Ala Arg Tyr Tyr Gln Leu Gln
130 135 140

Pro Met Val Arg Glu Leu Glu Arg Trp Gln Gln Glu Gln Glu Gln Arg
145 150 155 160

Arg Arg Ser Arg Ala Cys Asp Cys Leu Val Val Arg Val Thr Pro Asp
165 170 175

Leu Gly Glu Arg Ile Ala Leu Ser Gly Glu Lys Ala Leu Ile Glu Glu
180 185 190

Val Phe Pro Glu Thr Gly Asp Val Met Cys Asn Ser Val Asn Ala Gly
195 200 205

Trp Asn Gln Asp Pro Thr His Val Ile Arg Phe Pro Leu Asn Gly Tyr
 210 215 220

Cys Arg Leu Asn Ser Val Gln Asp Val Leu
 225 230

<210> 6

<211> 338

<212> PRT

<213> Drosophila melanogaster

<400> 6

Met Asp Arg Glu Arg Glu Arg Asp Val Lys Ala Leu Glu Pro Arg Asp
 1 5 10 15

Leu Ser Ser Thr Gly Arg Ile Tyr Ala Arg Ser Asp Ile Lys Ile Ser
 20 25 30

Ser Ser Pro Thr Val Ser Pro Thr Ile Ser Asn Ser Ser Ser Pro Thr
 35 40 45

Pro Thr Pro Pro Ala Ser Ser Ser Val Thr Pro Leu Gly Leu Pro Gly
 50 55 60

Ala Val Ala Ala Ala Ala Ala Ala Val Gly Gly Ala Ser Ser Ala Gly
 65 70 75 80

Ala Ser Ser Tyr Leu His Gly Asn His Lys Pro Ile Thr Gly Ile Pro
 85 90 95

Cys Val Ala Ala Ala Ser Arg Tyr Thr Ala Pro Val His Ile Asp Val
 100 105 110

Gly Gly Thr Ile Tyr Thr Ser Ser Leu Glu Thr Leu Thr Lys Tyr Pro
 115 120 125

Glu Ser Lys Leu Ala Lys Leu Phe Asn Gly Gln Ile Pro Ile Val Leu
 130 135 140

Asp Ser Leu Lys Gln His Tyr Phe Ile Asp Arg Asp Gly Gly Met Phe
 145 150 155 160

Arg His Ile Leu Asn Phe Met Arg Asn Ser Arg Leu Leu Ile Ala Glu
 165 170 175

Asp Phe Pro Asp Leu Glu Leu Leu Leu Glu Glu Ala Arg Tyr Tyr Glu
 180 185 190

Val Glu Pro Met Ile Lys Gln Leu Glu Ser Met Arg Lys Asp Arg Val
 195 200 205

Arg Asn Gly Asn Tyr Leu Val Ala Pro Pro Thr Pro Pro Ala Arg His
 210 215 220

~~Ile Lys Thr Ser Pro Arg Thr Ser Ala Ser Pro Glu Cys Asn Tyr Glu~~

225 230 235 240
 Val Val Ala Leu His Ile Ser Pro Asp Leu Gly Glu Arg Ile Met Leu
 245 250 255
 Ser Ala Glu Arg Ala Leu Leu Asp Glu Leu Phe Pro Glu Ala Ser Gln
 260 265 270
 Ala Thr Gln Ser Ser Arg Ser Gly Val Ser Trp Asn Gln Gly Asp Trp
 275 280 285
 Gly Gln Ile Ile Arg Phe Pro Leu Asn Gly Tyr Cys Lys Leu Asn Ser
 290 295 300
 Val Gln Val Leu Thr Arg Leu Leu Asn Ala Gly Phe Thr Ile Glu Ala
 305 310 315 320
 Ser Val Gly Gly Gln Gln Phe Ser Glu Tyr Leu Leu Ala Arg Arg Val
 325 330 335

Pro Met

<210> 7
 <211> 733
 <212> DNA
 <213> homo sapiens

<400> 7
 gggatccgga gcccaaattct tctgacaaaa ctacacatg cccaccgtgc ccagcacctg 60
 aattcgaggg tgcaccgtca gtcttctct tcccccaaa acccaaggac accctcatga 120
 tctcccgga tcttgaggtc acatgcgtgg tgggtgacgt aagccacgaa gaccctgagg 180
 tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca aagccgcggg 240
 aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg caccaggact 300
 ggctgaatgg caaggagtac aagtgaagg tctccaacaa agccctccca acccccatcg 360
 agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc 420
 catcccgga tgagctgacc aagaaccagg tcagcctgac ctgcctgggtc aaaggcttct 480
 atccaagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac aactacaaga 540
 ccacgcctcc cgtgctggac tccgacggct ctttcttct ctacagcaag ctcaccgtgg 600
 acaagagcag gtggcagcag gggaaagtct tctcatgctc cgtgatgcat gaggctctgc 660
 acaaccacta cagcagaag agcctctccc tgtctccggg taaatgagtg cgacggccgc 720
 gactctagag gat 733

<210> 8

<211> 724
 <212> DNA
 <213> homo sapiens

<220>
 <221> Unsure
 <222> (1)..(3)
 <223> wherein "N" is equal to "A", "G", "C", or "T".

<400> 8
 nnnagtgaag ctaatgtact ttgcacagtg ttagcaatta tcacccattc atcaggtatt 60
 aattcatttc gatcccaagg gcataggctt gatgtacaat aaggagttaa ggactgttaa 120
 ttctctgata aggttttggtt atagtcattt ctcaattctc accctctcca ggactacttc 180
 cagcaaccca gtctcctgcc atgtccgacc ccatcacgct gaacgtcggg gggaagctct 240
 atacaacctc actggcgacc ctgaccagct tccctgactc catgctagge gccatgttca 300
 gcgggaagat gcccaccaag agggacagcc agggcaactg cttcattgac cgtgacggca 360
 aagtgttccg ctatatctc aacttcctgc ggacctcca cttgacctg cctgaggact 420
 tccaggagat ggggctgctc cgcaggagg cgcacttcta ccagggtgcag cccctgattg 480
 aggccttgca ggagaaggaa gtggagctct ccaaggccga gaagaatgcc atgctcaaca 540
 tcacactgaa ccagcgtgtg cagacgggtcc acttcactgt gcgcgaggca cccagatct 600
 acagcctctc ctcttcacgc atggaggtct tcaacgcaa catcttcage acctcctgcc 660
 tcttctcaa gctccttggc tctaagctct tctactgctc caatggcaat ctctcctcca 720
 tcac 724

<210> 9
 <211> 74
 <212> DNA
 <213> homo sapiens

<400> 9
 ttgaggatat agcgaacac tttgccgtca cggatcaatga agcagttgcc ctggctgtcc 60
 ctcttggtgg gcat 74

<210> 10
 <211> 20
 <212> DNA
 <213> homo sapiens

<400> 10
 atacaacctc actggcgacc 20

<210> 11
 <211> 20
 <212> DNA
 <213> homo sapiens

<400> 11
 ccattctcctg gaagtcctca

20

<210> 12
 <211> 99
 <212> PRT
 <213> homo sapiens

<400> 12

Asp Pro Ile Thr Leu Asn Val Gly Gly Lys Leu Tyr Thr Thr Ser Leu
 1 5 10 15

Ala Thr Leu Thr Ser Phe Pro Asp Ser Met Leu Gly Ala Met Phe Ser
 20 25 30

Gly Lys Met Pro Thr Lys Arg Asp Ser Gln Gly Asn Cys Phe Ile Asp
 35 40 45

Arg Asp Gly Lys Val Phe Arg Tyr Ile Leu Asn Phe Leu Arg Thr Ser
 50 55 60

His Leu Asp Leu Pro Glu Asp Phe Gln Glu Met Gly Leu Leu Arg Arg
 65 70 75 80

Glu Ala Asp Phe Tyr Gln Val Gln Pro Leu Ile Glu Ala Leu Gln Glu
 85 90 95

Lys Glu Val

<210> 13
 <211> 14
 <212> PRT
 <213> homo sapiens

<400> 13

Phe Cys Lys Gln Arg Asn Lys Ser Leu Gly Thr Tyr Pro Gly
 1 5 10

<210> 14
 <211> 14
 <212> PRT
 <213> homo sapiens

<400> 14

Lys Asn Ala Met Leu Asn Ile Thr Leu Asn Gln Arg Val Gln
 1 5 10

<210> 15
<211> 14
<212> PRT
<213> homo sapiens

<400> 15

Tyr Cys Ser Asn Gly Asn Leu Ser Ser Ile Thr Ser His Leu
1 5 10

<210> 16
<211> 13
<212> PRT
<213> homo sapiens

<400> 16

Asp Thr Arg Phe Phe Ser Cys Arg Glu Gly Leu Leu Pro
1 5 10

<210> 17
<211> 13
<212> PRT
<213> homo sapiens

<400> 17

Leu Gly Ala Met Phe Ser Gly Lys Met Pro Thr Lys Arg
1 5 10

<210> 18
<211> 13
<212> PRT
<213> homo sapiens

<400> 18

Ser Gly Lys Met Pro Thr Lys Arg Asp Ser Gln Gly Asn
1 5 10

<210> 19
<211> 13
<212> PRT
<213> homo sapiens

<400> 19

Gln Thr Val His Phe Thr Val Arg Glu Ala Pro Gln Ile
1 5 10

<210> 20
<211> 26
<212> PRT
<213> homo sapiens

<400> 20

Gly Thr Tyr Pro Gly Val Pro Gly Asn Ala Leu Trp Leu Leu Thr Ser
 1 5 10 15

Pro Ala Cys Asn Ala Leu Ser Thr Ser Ala
 20 25

<210> 21
 <211> 25
 <212> PRT
 <213> homo sapiens

<400> 21

Val Phe Asn Ala Asn Ile Phe Ser Thr Ser Cys Leu Phe Leu Lys Leu
 1 5 10 15

Leu Gly Ser Lys Leu Phe Tyr Cys Ser
 20 25

<210> 22
 <211> 8
 <212> PRT
 <213> bacteriophage T7

<400> 22

Asp Tyr Lys Asp Asp Asp Asp Lys
 1 5

<210> 23
 <211> 2154
 <212> DNA
 <213> homo sapiens

<220>
 <221> CDS
 <222> (1)..(1029)

<400> 23

atg acg atg gcg gtt ttg cgg aat aga aaa ggg gga aag gga cca ctc 48
 Met Thr Met Ala Val Leu Arg Asn Arg Lys Gly Gly Lys Gly Pro Leu
 1 5 10 15

agg cgc cgg ccg ctg gcg ctg cct gct ctt cga ctg ggc gag ctt cct 96
 Arg Arg Arg Pro Leu Ala Leu Pro Ala Leu Arg Leu Gly Glu Leu Pro
 20 25 30

gcc aat cag ggc gga acc agc gcg gcg tcg gcc agt agc ggg agg cgg 144
 Ala Asn Gln Gly Gly Thr Ser Ala Ala Ser Ala Ser Ser Gly Arg Arg
 35 40 45

tcg ggt cag gcc cca gct ggg cgc gag cgg gtc ggc gtt gag gga gcc 192
 Ser Gly Gln Ala Pro Ala Gly Arg Glu Arg Val Gly Val Glu Gly Ala
 50 55 60

-----aac-gcc-ctc-ccg-eet-geg-eac-tgc-ctc-tcg-ccc-ccc-tcc-ggc-cag-ccc-----240-----

Thr	Ala	Leu	Pro	Pro	Ala	His	Cys	Leu	Ser	Pro	Pro	Ser	Gly	Gln	Pro	
65					70					75					80	
gca	gcc	ggc	cgc	gtc	atg	cca	ggc	gct	gct	cgg	cga	gcc	aga	ggg	atg	288
Ala	Ala	Gly	Arg	Val	Met	Pro	Gly	Ala	Ala	Arg	Arg	Ala	Arg	Gly	Met	
				85					90					95		
gtg	gta	gtc	acg	ggg	cgg	gag	cca	gac	agc	cgt	cgt	cag	gac	ggg	gcc	336
Val	Val	Val	Thr	Gly	Arg	Glu	Pro	Asp	Ser	Arg	Arg	Gln	Asp	Gly	Ala	
			100					105					110			
atg	tcc	agc	tct	gac	gcc	gaa	gac	gac	ttt	ctg	gag	cgc	gcc	acg	cgc	384
Met	Ser	Ser	Ser	Asp	Ala	Glu	Asp	Asp	Phe	Leu	Glu	Pro	Ala	Thr	Pro	
		115					120					125				
acg	gcc	acg	cag	gcg	ggg	cac	gcg	ctg	ccc	ctg	ctg	cca	cag	gag	ttt	432
Thr	Ala	Thr	Gln	Ala	Gly	His	Ala	Leu	Pro	Leu	Leu	Pro	Gln	Glu	Phe	
	130					135				140						
cct	gag	gtt	gtt	ccc	ctt	aac	atc	gga	ggg	gct	cac	ttc	act	aca	cgc	480
Pro	Glu	Val	Val	Pro	Leu	Asn	Ile	Gly	Gly	Ala	His	Phe	Thr	Thr	Arg	
145					150				155						160	
ctg	tcc	aca	ctg	cgg	tgc	tac	gaa	gac	acc	atg	ttg	gca	gcc	atg	ttc	528
Leu	Ser	Thr	Leu	Arg	Cys	Tyr	Glu	Asp	Thr	Met	Leu	Ala	Ala	Met	Phe	
				165					170					175		
agt	ggg	cgg	cac	tac	atc	ccc	aca	gac	tcc	gag	ggc	cgg	tac	ttc	atc	576
Ser	Gly	Arg	His	Tyr	Ile	Pro	Thr	Asp	Ser	Glu	Gly	Arg	Tyr	Phe	Ile	
			180					185					190			
gac	cga	gat	ggc	aca	cac	ttt	gga	gat	gtg	ctg	aat	ttc	ctg	cgc	tca	624
Asp	Arg	Asp	Gly	Thr	His	Phe	Gly	Asp	Val	Leu	Asn	Phe	Leu	Arg	Ser	
		195					200				205					
ggg	gac	ctc	cca	ccc	agg	gag	cgt	gtt	cga	gct	gtg	tac	aaa	gag	gcc	672
Gly	Asp	Leu	Pro	Pro	Arg	Glu	Arg	Val	Arg	Ala	Val	Tyr	Lys	Glu	Ala	
	210					215				220						
cag	tac	tat	gcc	atc	ggg	ccc	ctc	ctg	gag	cag	ctg	gag	aac	atg	cag	720
Gln	Tyr	Tyr	Ala	Ile	Gly	Pro	Leu	Leu	Glu	Gln	Leu	Glu	Asn	Met	Gln	
225					230				235					240		
cca	ctg	aag	ggc	gag	aag	gtg	cgc	caa	gcg	ttt	ctg	gga	ctc	atg	ccc	768
Pro	Leu	Lys	Gly	Glu	Lys	Val	Arg	Gln	Ala	Phe	Leu	Gly	Leu	Met	Pro	
				245				250						255		
tat	tac	aaa	gac	cac	ttg	gag	cgg	att	gtg	gag	atc	gcc	cgg	ctg	cgt	816
Tyr	Tyr	Lys	Asp	His	Leu	Glu	Arg	Ile	Val	Glu	Ile	Ala	Arg	Leu	Arg	
			260				265					270				
gcg	gtc	cag	cgg	aag	gcc	cgc	ttt	gcc	aag	ctc	aag	agc	ttg	aca	cct	864
Ala	Val	Gln	Arg	Lys	Ala	Arg	Phe	Ala	Lys	Leu	Lys	Ser	Leu	Thr	Pro	
		275				280				285						
tcc	tgg	cta	atg	agt	gtc	ctc	atc	aag	atg	ccc	cct	gga	gtc	aca	tca	912
Ser	Trp	Leu	Met	Ser	Val	Leu	Ile	Lys	Met	Pro	Pro	Gly	Val	Thr	Ser	

290	295	300	
tgg att aac gca gaa agg cgg ctg tat ttg gaa act ccc att ggt cca			960
Trp Ile Asn Ala Glu Arg Arg Leu Tyr Leu Glu Thr Pro Ile Gly Pro			
305	310	315	320
gag aga cag aac aat gag aag aaa tcc cct gtc cag ttg cct gca gga			1008
Glu Arg Gln Asn Asn Glu Lys Lys Ser Pro Val Gln Leu Pro Ala Gly			
325	330		335
gta ttc caa cac ttc atg ggc tagaggattc cattgagatg gggtttacgt			1059
Val Phe Gln His Phe Met Gly			
340			
cttgattttg aacacctgtc agcactgttc tctgtttgca tggcaattct gaccctttta			1119
tggcaacaac acccctggga caaccagat ttgtagattg agatccaaag gtagaatttc			1179
cagacagtcc aaccaaggta tcaagtgatg tttccagagt ggaaggctct caccgtgtcc			1239
caggatttct ggggtttgta agcagtactg gccatttgtg accctgtttt ttacctaatc			1299
attctgtctt tttaggacat ggttttaccc gatccctggc aaaggatcca gaattccaat			1359
agctgaaaac cctgttatag cttttctcct attctgcctt acccaagaca cacttgaacc			1419
cctcagtaag gctatagaga gggccatgag caggggcagc ctctcccttg tttctacagc			1479
tccatgatga ggggttgact gagggcagca atccttgtag gtgtgacagt tgcaatataa			1539
ttaacagttt caagatctag aggtacctt tgaaagaacc ccttcaggga tatctatcca			1599
cagtagcctg gagcagccaa ggtgaacctg agattttgac ccacacaata agggggggcc			1659
attctttttc aaatatatttg gcttcagaat acacttcatt acacatgcaa atattgagag			1719
attaacagaa attccagctc ttatgcctaa ctgagaagag ccaactgcaag ttgcagttag			1779
gtacccatgt gcagcagagg ccagctgaat ccagagctt cccaaagtgg acaccagcgg			1839
ggactattcc tgatgtccca cccaagagag gaagatgagc tgaggcgctc ttgctctgcc			1899
caaatgcac ccatgtgcat tcacgtgtca cccattcaaa ataacatggc attcttggaa			1959
ccttgtatct gacatgtaag accagcctac acattggggg gggcgcagg gctcacactt			2019
gtaatcctag cactttggaa ggctgaggtg ggcagattgc ttgagcacag gagttccaga			2079
ccagcctgag caacatggcg aaatcctgtc tcttcaagaa ataaaataat aataataata			2139
aaaaaaaaa aaaaa			2154

<210> 24

<211> 343

<212> PRT

<213> homo sapiens

<400> 24

Met Thr Met Ala Val Leu Arg Asn Arg Lys Gly Gly Lys Gly Pro Leu
1 5 10 15

Arg Arg Arg Pro Leu Ala Leu Pro Ala Leu Arg Leu Gly Glu Leu Pro
20 25 30

Ala Asn Gln Gly Gly Thr Ser Ala Ala Ser Ala Ser Ser Gly Arg Arg
35 40 45

Ser Gly Gln Ala Pro Ala Gly Arg Glu Arg Val Gly Val Glu Gly Ala
50 55 60

Thr Ala Leu Pro Pro Ala His Cys Leu Ser Pro Pro Ser Gly Gln Pro
65 70 75 80

Ala Ala Gly Arg Val Met Pro Gly Ala Ala Arg Arg Ala Arg Gly Met
85 90 95

Val Val Val Thr Gly Arg Glu Pro Asp Ser Arg Arg Gln Asp Gly Ala
100 105 110

Met Ser Ser Ser Asp Ala Glu Asp Asp Phe Leu Glu Pro Ala Thr Pro
115 120 125

Thr Ala Thr Gln Ala Gly His Ala Leu Pro Leu Leu Pro Gln Glu Phe
130 135 140

Pro Glu Val Val Pro Leu Asn Ile Gly Gly Ala His Phe Thr Thr Arg
145 150 155 160

Leu Ser Thr Leu Arg Cys Tyr Glu Asp Thr Met Leu Ala Ala Met Phe
165 170 175

Ser Gly Arg His Tyr Ile Pro Thr Asp Ser Glu Gly Arg Tyr Phe Ile
180 185 190

Asp Arg Asp Gly Thr His Phe Gly Asp Val Leu Asn Phe Leu Arg Ser
195 200 205

Gly Asp Leu Pro Pro Arg Glu Arg Val Arg Ala Val Tyr Lys Glu Ala
210 215 220

Gln Tyr Tyr Ala Ile Gly Pro Leu Leu Glu Gln Leu Glu Asn Met Gln
 225 230 235 240

Pro Leu Lys Gly Glu Lys Val Arg Gln Ala Phe Leu Gly Leu Met Pro
 245 250 255

Tyr Tyr Lys Asp His Leu Glu Arg Ile Val Glu Ile Ala Arg Leu Arg
 260 265 270

Ala Val Gln Arg Lys Ala Arg Phe Ala Lys Leu Lys Ser Leu Thr Pro
 275 280 285

Ser Trp Leu Met Ser Val Leu Ile Lys Met Pro Pro Gly Val Thr Ser
 290 295 300

Trp Ile Asn Ala Glu Arg Arg Leu Tyr Leu Glu Thr Pro Ile Gly Pro
 305 310 315 320

Glu Arg Gln Asn Asn Glu Lys Lys Ser Pro Val Gln Leu Pro Ala Gly
 325 330 335

Val Phe Gln His Phe Met Gly
 340

<210> 25
 <211> 225
 <212> PRT
 <213> homo sapiens

<400> 25

Met Ser Thr Val Val Glu Leu Asn Val Gly Gly Glu Phe His Thr Thr
 1 5 10 15

Thr Leu Gly Thr Leu Arg Lys Phe Pro Gly Ser Lys Leu Ala Glu Met
 20 25 30

Phe Ser Ser Leu Ala Lys Ala Ser Thr Asp Ala Glu Gly Arg Phe Phe
 35 40 45

Ile Asp Arg Pro Ser Thr Tyr Phe Arg Pro Ile Leu Asp Tyr Leu Arg
 50 55 60

Thr Gly Gln Val Pro Thr Gln His Ile Pro Glu Val Tyr Arg Glu Ala
 65 70 75 80

-----Gln-Phe-Tyr-Glu-Ile-Lys-Pro-Leu-Val-Lys-Leu-Leu-Glu-Asp-Met-Pro-----

85					90					95					
Gln	Ile	Phe	Gly	Glu	Gln	Val	Ser	Arg	Lys	Gln	Phe	Leu	Leu	Gln	Val
			100					105					110		
Pro	Gly	Tyr	Ser	Glu	Asn	Leu	Glu	Leu	Met	Val	Arg	Leu	Ala	Arg	Ala
		115					120					125			
Glu	Ala	Ile	Thr	Ala	Arg	Lys	Ser	Ser	Val	Leu	Val	Cys	Leu	Val	Glu
	130					135					140				
Thr	Glu	Glu	Gln	Asp	Ala	Tyr	Tyr	Ser	Glu	Val	Leu	Cys	Phe	Leu	Gln
	145					150					155				160
Asp	Lys	Lys	Met	Phe	Lys	Ser	Val	Val	Lys	Phe	Gly	Pro	Trp	Lys	Ala
				165					170					175	
Val	Leu	Asp	Asn	Ser	Asp	Leu	Met	His	Cys	Leu	Glu	Met	Asp	Ile	Lys
			180					185					190		
Ala	Gln	Gly	Tyr	Lys	Val	Phe	Ser	Lys	Phe	Tyr	Leu	Thr	Tyr	Pro	Thr
		195					200					205			
Lys	Arg	Asn	Glu	Phe	His	Phe	Asn	Ile	Tyr	Ser	Phe	Thr	Phe	Thr	Trp
	210					215					220				

Trp
225

<210> 26
 <211> 313
 <212> PRT
 <213> homo sapiens

<400> 26

Met	Glu	Glu	Met	Ser	Gly	Glu	Ser	Val	Val	Ser	Ser	Ala	Val	Pro	Ala
1				5					10					15	
Ala	Ala	Thr	Arg	Thr	Thr	Ser	Phe	Lys	Gly	Thr	Ser	Pro	Ser	Ser	Lys
			20					25					30		
Tyr	Val	Lys	Leu	Asn	Val	Gly	Gly	Ala	Leu	Tyr	Tyr	Thr	Thr	Met	Gln
		35					40					45			
Thr	Leu	Thr	Lys	Gln	Asp	Thr	Met	Leu	Lys	Ala	Met	Phe	Ser	Gly	Arg
	50					55					60				
Met	Glu	Val	Leu	Thr	Asp	Ser	Glu	Gly	Trp	Ile	Leu	Ile	Asp	Arg	Cys
65					70					75					80
Gly	Lys	His	Phe	Gly	Thr	Ile	Leu	Asn	Tyr	Leu	Arg	Asp	Gly	Ala	Val
				85					90					95	
Pro	Leu	Pro	Glu	Ser	Arg	Arg	Glu	Ile	Glu	Glu	Leu	Leu	Ala	Glu	Ala
			100					105						110	

Lys Tyr Tyr Leu Val Gln Gly Leu Val Glu Glu Cys Gln Ala Ala Leu
 115 120 125
 Gln Asn Lys Asp Thr Tyr Glu Pro Phe Cys Lys Val Pro Val Ile Thr
 130 135 140
 Ser Ser Lys Glu Glu Gln Lys Leu Ile Ala Thr Ser Asn Lys Pro Ala
 145 150 155 160
 Val Lys Leu Leu Tyr Asn Arg Ser Asn Asn Lys Tyr Ser Tyr Thr Ser
 165 170 175
 Asn Ser Asp Asp Asn Met Leu Lys Asn Ile Glu Leu Phe Asp Lys Leu
 180 185 190
 Ser Leu Arg Phe Asn Gly Arg Val Leu Phe Ile Lys Asp Val Ile Gly
 195 200 205
 Asp Glu Ile Cys Cys Trp Ser Phe Tyr Gly Gln Gly Arg Lys Ile Ala
 210 215 220
 Glu Val Cys Cys Thr Ser Ile Val Tyr Ala Thr Glu Lys Lys Gln Thr
 225 230 235 240
 Lys Val Glu Phe Pro Glu Ala Arg Ile Tyr Glu Glu Thr Leu Asn Ile
 245 250 255
 Leu Leu Tyr Glu Ala Gln Asp Gly Arg Gly Pro Asp Asn Ala Leu Leu
 260 265 270
 Glu Ala Thr Gly Gly Ala Ala Gly Arg Ser His His Leu Asp Glu Asp
 275 280 285
 Glu Glu Arg Glu Arg Ile Glu Arg Val Arg Arg Ile His Ile Lys Arg
 290 295 300
 Pro Asp Asp Arg Ala His Leu His Gln
 305 310

<210> 27
 <211> 301
 <212> PRT
 <213> Drosophila melanogaster

<400> 27

Met Ser Glu Ser Met Ser Gly Asp His Lys Ile Leu Leu Lys Gly His
 1 5 10 15
 Ser Ser Gln Tyr Leu Lys Leu Asn Val Gly Gly His Leu Tyr Tyr Thr
 20 25 30
 Thr Ile Gly Thr Leu Thr Lys Asn Asn Asp Thr Met Leu Ser Ala Met
 35 40 45
 Phe Ser Gly Arg Met Glu Val Leu Thr Asp Ser Glu Gly Trp Ile Leu
 50 55 60

Ile Asp Arg Cys Gly Asn His Phe Gly Ile Ile Leu Asn Tyr Leu Arg
 65 70 75 80
 Asp Gly Thr Val Pro Leu Pro Glu Thr Asn Lys Glu Ile Ala Glu Leu
 85 90 95
 Leu Ala Glu Ala Lys Tyr Tyr Cys Ile Thr Glu Leu Ala Ile Ser Cys
 100 105 110
 Glu Arg Ala Leu Tyr Ala His Gln Glu Pro Lys Pro Ile Cys Arg Ile
 115 120 125
 Pro Leu Ile Thr Ser Gln Lys Glu Glu Gln Leu Leu Leu Ser Val Ser
 130 135 140
 Leu Lys Pro Ala Val Ile Leu Val Val Gln Arg Gln Asn Asn Lys Tyr
 145 150 155 160
 Ser Tyr Thr Ser Thr Ser Asp Asp Asn Leu Leu Lys Asn Ile Glu Leu
 165 170 175
 Phe Asp Lys Leu Ser Leu Arg Phe Asn Glu Arg Ile Leu Phe Ile Lys
 180 185 190
 Asp Val Ile Gly Pro Ser Glu Ile Cys Cys Trp Ser Phe Tyr Gly His
 195 200 205
 Gly Lys Lys Val Ala Glu Val Cys Cys Thr Ser Ile Val Tyr Ala Thr
 210 215 220
 Asp Arg Lys His Thr Lys Val Glu Phe Pro Glu Ala Arg Ile Tyr Glu
 225 230 235 240
 Glu Thr Leu Gln Val Leu Leu Tyr Glu Asn Arg Asn Ala Pro Asp Gln
 245 250 255
 Glu Leu Met Gln Ala Thr Ser Ser Ala Arg Val Gly Ser Ala Ser Gly
 260 265 270
 Thr Ser Ile Asn Gln Tyr Thr Ser Asp Glu Glu Glu Glu Arg Thr Gly
 275 280 285
 Leu Ala Arg Leu Arg Ser Asn Lys Arg Asn Asn Pro Ser
 290 295 300

<210> 28
 <211> 221
 <212> PRT
 <213> Caenorhabditis elegans

<400> 28

Met Glu Pro Ser Thr Ile Val Lys Leu Asp Val Gly Gly Lys Ile Phe
 1 5 10 15

~~Lys Thr Thr Ile Phe Thr Leu Cys Lys His Asp Ser Met Leu Lys Thr~~

20					25					30					
Met	Phe	Cys	Thr	Asp	Val	Pro	Val	Thr	Lys	Asn	Glu	Glu	Gly	Ser	Val
		35					40					45			
Phe	Ile	Asp	Arg	Asp	Ser	Lys	His	Phe	Arg	Leu	Ile	Leu	Asn	Phe	Leu
	50					55					60				
Arg	Asp	Gly	Gln	Ile	Ala	Leu	Pro	Asp	Ser	Asp	Arg	Glu	Val	Arg	Glu
65					70					75					80
Val	Leu	Ala	Glu	Ala	Ser	Tyr	Phe	Leu	Leu	Asp	Pro	Leu	Ile	Glu	Leu
				85					90					95	
Cys	Gly	Glu	Arg	Leu	Glu	Gln	Ser	Leu	Asn	Pro	Tyr	Tyr	His	Leu	Val
			100					105					110		
Ser	Thr	Val	Leu	Glu	Ala	Arg	Lys	Ile	Ile	Phe	Ala	Thr	Glu	Lys	Pro
		115					120					125			
Ile	Val	Val	Leu	Arg	Leu	Pro	Val	Tyr	Ile	Ala	Thr	Ser	Gly	Asn	Gln
	130					135					140				
Ser	Tyr	Tyr	Phe	Ser	Glu	Thr	Lys	Phe	Arg	Glu	Leu	Ser	Glu	Glu	Tyr
145					150					155					160
His	Lys	His	Val	Ala	Phe	Ile	Leu	Ile	Thr	Glu	Pro	Glu	Phe	Asn	Glu
			165					170						175	
Asp	Cys	Ser	Trp	Ser	Phe	Phe	Leu	Arg	Ala	Lys	Lys	Ile	Thr	Ala	Arg
		180						185					190		
Ile	Lys	Gly	Pro	Met	Asp	Cys	Asn	Leu	Val	Glu	Glu	Cys	Met	Pro	Lys
	195						200					205			
Thr	Val	Glu	Arg	Arg	Arg	Glu	Lys	Lys	Thr	Trp	His	His			
	210					215					220				

<210> 29
 <211> 583
 <212> DNA
 <213> homo sapiens

<400> 29
 gctatgaggg ttagaatggg taggacttgg cagatgatga gggtggggca gagggaggag 60
 agagaagaaa gtgttcagat ggacccgtgg gcttgagtga ctgaatgaat ggtgtggcac 120
 caatcagacc ccagggattg aagatggagc agccccagct ctcattcccc gttgcctgcc 180
 tgagagccct ggtgatttct ttccagtttc ctgaggttgt tccccttaac atcgagggg 240
 ctcacttcac tacacgctg tccacactgc ggtgctacga agacaccatg ttggcagcca 300
 tgttcagtgg gcggcactac atccccacgg actccgaggg ccggtacttc atcgaccgag 360
 -----atggcacaca-ctttgggtat-gtctctct-ctacaatcaa-ctttgtagtc-ctagcagggtg----- 420

attagcgtag gcttgagtat gggaccttga tatcttccat agtacctaga agaggagata 480
gcatattgat gaaatttaat aaatgggttt attgaaagag atcaattttt tttttttttt 540
ttgccaaagg agacaaagac agccagagaa attcgaaata aca 583

<210> 30
<211> 80
<212> DNA
<213> homo sapiens

<400> 30
gatgaagtac cggccctcgg agtccgtggg gatgtagtgc cgcccactga acatggctgc 60
caacatgggtg ttttcgtagc 80

<210> 31
<211> 20
<212> DNA
<213> homo sapiens

<400> 31
tgttcccctt aacatcggag 20

<210> 32
<211> 20
<212> DNA
<213> homo sapiens

<400> 32
catacccaaa gtgtgtgcca 20

<210> 33
<211> 13
<212> PRT
<213> homo sapiens

<400> 33

Ala Ala Ser Ala Ser Ser Gly Arg Arg Ser Gly Gln Ala
1 5 10

<210> 34
<211> 13
<212> PRT
<213> homo sapiens

<400> 34

Gly Met Val Val Val Thr Gly Arg Glu Pro Asp Ser Arg
1 5 10

<210> 35
<211> 13
<212> PRT
<213> homo sapiens

<400> 35

Gly Arg Glu Pro Asp Ser Arg Arg Gln Asp Gly Ala Met
1 5 10

<210> 36
<211> 13
<212> PRT
<213> homo sapiens

<400> 36

Gly Gly Ala His Phe Thr Thr Arg Leu Ser Thr Leu Arg
1 5 10

<210> 37
<211> 13
<212> PRT
<213> homo sapiens

<400> 37

Thr Thr Arg Leu Ser Thr Leu Arg Cys Tyr Glu Asp Thr
1 5 10

<210> 38
<211> 13
<212> PRT
<213> homo sapiens

<400> 38

Leu Ala Ala Met Phe Ser Gly Arg His Tyr Ile Pro Thr
1 5 10

<210> 39
<211> 96
<212> PRT
<213> homo sapiens

<400> 39

Glu Val Val Pro Leu Asn Ile Gly Gly Ala His Phe Thr Thr Arg Leu
1 5 10 15

Ser Thr Leu Arg Cys Tyr Glu Asp Thr Met Leu Ala Ala Met Phe Ser
20 25 30

Gly Arg His Tyr Ile Pro Thr Asp Ser Glu Gly Arg Tyr Phe Ile Asp
35 40 45

-----Arg-Asp-Gly-Thr-His-Phe-Gly-Asp-Val-Leu-Asn-Phe-Leu-Arg-Ser-Gly-----

50 55 60
 Asp Leu Pro Pro Arg Glu Arg Val Arg Ala Val Tyr Lys Glu Ala Gln
 65 70 75 80

Tyr Tyr Ala Ile Gly Pro Leu Leu Glu Gln Leu Glu Asn Met Gln Pro
 85 90 95

<210> 40
 <211> 25
 <212> PRT
 <213> homo sapiens

<400> 40

Ala Lys Leu Lys Ser Leu Thr Pro Ser Trp Leu Met Ser Val Leu Ile
 1 5 10 15

Lys Met Pro Pro Gly Val Thr Ser Trp
 20 25

<210> 41
 <211> 39
 <212> DNA
 <213> homo sapiens

<400> 41
 gcagcagcgg ccgcggacca ctcaggcgcc ggccgctgg 39

<210> 42
 <211> 38
 <212> DNA
 <213> homo sapiens

<400> 42
 gcagcagtcg acgcccatga agtggttgaa tactcctg 38

<210> 43
 <211> 49
 <212> DNA
 <213> homo sapiens

<400> 43
 gcagcagcgg ccgcatgacg atggcggttt tgcggaatag aaaaggggg 49

<210> 44
 <211> 40
 <212> DNA
 <213> homo sapiens

<400> 44
 gcagcagtcg acctggaccg cacgcagccg ggcgatctcc 40

<210> 45
 <211> 21
 <212> DNA
 <213> Homo sapiens

 <400> 45
 gtgccgcatt tatccatctg t 21

 <210> 46
 <211> 23
 <212> DNA
 <213> Homo sapiens

 <400> 46
 tggaggtagc ctcttggtct cat 23

 <210> 47
 <211> 24
 <212> DNA
 <213> Homo sapiens

 <400> 47
 ccatcctctc caccagggcc ttct 24

 <210> 48
 <211> 18
 <212> DNA
 <213> Homo sapiens

 <400> 48
 tgccccctgg agtcacat 18

 <210> 49
 <211> 20
 <212> DNA
 <213> Homo sapiens

 <400> 49
 ggaccaatgg gagttttcaa 20

 <210> 50
 <211> 25
 <212> DNA
 <213> Homo sapiens

 <400> 50
 cagccgcctt tctgcgttaa tccat 25

 <210> 51
 <211> 14
 <212> PRT

<213> homo sapiens

<400> 51

Ala Ala Ser Ala Ser Ser Gly Arg Arg Ser Gly Gln Ala Pro
1 5 10

<210> 52

<211> 20

<212> DNA

<213> Drosophila melanogaster

<400> 52

atgaggcttg gatcagcttt 20

<210> 53

<211> 20

<212> DNA

<213> Drosophila melanogaster

<400> 53

cctgaagcct gacattccat 20

<210> 54

<211> 21

<212> DNA

<213> Drosophila melanogaster

<400> 54

actgcagccg attcattaat g 21

<210> 55

<211> 48

<212> DNA

<213> Drosophila melanogaster

<400> 55

gaattaatac gactcactat agggagatat catacacata cgatttag 48

<210> 56

<211> 48

<212> DNA

<213> Drosophila melanogaster

<400> 56

gaattaatac gactcactat agggagacat gattacgcca agctcgaa 48

<210> 57

<211> 21

<212> DNA

<213> Drosophila melanogaster

<400> 57
 tgtaaaacga cggccagtga a 21

<210> 58
 <211> 23
 <212> DNA
 <213> Homo sapiens

<400> 58
 caggtgcagc tggcgcagtc tgg 23

<210> 59
 <211> 23
 <212> DNA
 <213> Homo sapiens

<400> 59
 caggtcaact taaggagtc tgg 23

<210> 60
 <211> 23
 <212> DNA
 <213> Homo sapiens

<400> 60
 gaggtgcagc tggcgcagtc tgg 23

<210> 61
 <211> 23
 <212> DNA
 <213> Homo sapiens

<400> 61
 caggtgcagc tgcaggagtc ggg 23

<210> 62
 <211> 23
 <212> DNA
 <213> Homo sapiens

<400> 62
 gaggtgcagc tggcgcagtc tgc 23

<210> 63
 <211> 23
 <212> DNA
 <213> Homo sapiens

<400> 63
 caggtacagc tgcagcagtc agg 23

<210> 64
 <211> 24
 <212> DNA
 <213> Homo sapiens

 <400> 64
 tgaggagacg gtgaccaggg tgcc 24

 <210> 65
 <211> 24
 <212> DNA
 <213> Homo sapiens

 <400> 65
 tgaagagacg gtgaccattg tccc 24

 <210> 66
 <211> 24
 <212> DNA
 <213> Homo sapiens

 <400> 66
 tgaggagacg gtgaccaggg ttcc 24

 <210> 67
 <211> 24
 <212> DNA
 <213> Homo sapiens

 <400> 67
 tgaggagacg gtgaccgtgg tccc 24

 <210> 68
 <211> 23
 <212> DNA
 <213> Homo sapiens

 <400> 68
 gacatccaga tgacccagtc tcc 23

 <210> 69
 <211> 23
 <212> DNA
 <213> Homo sapiens

 <400> 69
 gatgttgtga tgactcagtc tcc 23

 <210> 70
 <211> 23

<212> DNA
 <213> Homo sapiens

 <400> 70
 gatattgtga tgactcagtc tcc 23

 <210> 71
 <211> 23
 <212> DNA
 <213> Homo sapiens

 <400> 71
 gaaattgtgt tgacgcagtc tcc 23

 <210> 72
 <211> 23
 <212> DNA
 <213> Homo sapiens

 <400> 72
 gacatcgtga tgacccagtc tcc 23

 <210> 73
 <211> 23
 <212> DNA
 <213> Homo sapiens

 <400> 73
 gaaacgacac tcacgcagtc tcc 23

 <210> 74
 <211> 23
 <212> DNA
 <213> Homo sapiens

 <400> 74
 gaaattgtgc tgactcagtc tcc 23

 <210> 75
 <211> 23
 <212> DNA
 <213> Homo sapiens

 <400> 75
 cagtctgtgt tgacgcagcc gcc 23

 <210> 76
 <211> 23
 <212> DNA
 <213> Homo sapiens

<400> 76	
cagtctgccc tgactcagcc tgc	23
<210> 77	
<211> 23	
<212> DNA	
<213> Homo sapiens	
<400> 77	
tcctatgtgc tgactcagcc acc	23
<210> 78	
<211> 23	
<212> DNA	
<213> Homo sapiens	
<400> 78	
tcttctgagc tgactcagga ccc	23
<210> 79	
<211> 23	
<212> DNA	
<213> Homo sapiens	
<400> 79	
cacgttatac tgactcaacc gcc	23
<210> 80	
<211> 23	
<212> DNA	
<213> Homo sapiens	
<400> 80	
caggctgtgc tcactcagcc gtc	23
<210> 81	
<211> 23	
<212> DNA	
<213> Homo sapiens	
<400> 81	
aattttatgc tgactcagcc cca	23
<210> 82	
<211> 24	
<212> DNA	
<213> Homo sapiens	
<400> 82	
acgtttgatt tccaccttgg tccc	24

<210> 83
 <211> 24
 <212> DNA
 <213> Homo sapiens

 <400> 83
 acgtttgatc tccagcttgg tccc 24

 <210> 84
 <211> 24
 <212> DNA
 <213> Homo sapiens

 <400> 84
 acgtttgata tccactttgg tccc 24

 <210> 85
 <211> 24
 <212> DNA
 <213> Homo sapiens

 <400> 85
 acgtttgatc tccaccttgg tccc 24

 <210> 86
 <211> 24
 <212> DNA
 <213> Homo sapiens

 <400> 86
 acgtttaatc tccagtcgtg tccc 24

 <210> 87
 <211> 23
 <212> DNA
 <213> Homo sapiens

 <400> 87
 cagtctgtgt tgacgcagcc gcc 23

 <210> 88
 <211> 23
 <212> DNA
 <213> Homo sapiens

 <400> 88
 cagtctgccc tgactcagcc tgc 23

 <210> 89
 <211> 23

<212> DNA
 <213> Homo sapiens

 <400> 89
 tcctatgtgc tgactcagcc acc 23

 <210> 90
 <211> 23
 <212> DNA
 <213> Homo sapiens

 <400> 90
 tcttctgagc tgactcagga ccc 23

 <210> 91
 <211> 23
 <212> DNA
 <213> Homo sapiens

 <400> 91
 cacgttatac tgactcaacc gcc 23

 <210> 92
 <211> 23
 <212> DNA
 <213> Homo sapiens

 <400> 92
 caggctgtgc tcactcagcc gtc 23

 <210> 93
 <211> 23
 <212> DNA
 <213> Homo sapiens

 <400> 93
 aattttatgc tgactcagcc cca 23

 <210> 94
 <211> 39
 <212> DNA
 <213> Homo sapiens

 <400> 94
 gcagcagcgg ccgctccgac cccatcacgc tgaacgtcg 39

 <210> 95
 <211> 37
 <212> DNA
 <213> Homo sapiens

<400> 95
gcagcagtcg accctgtacc gtattaatcg aataatc

37

<210> 96
<211> 39
<212> DNA
<213> Homo sapiens

<400> 96
gcagcagcgg ccgcatgacc gggagccatg acgtcatcg

39

<210> 97
<211> 37
<212> DNA
<213> Homo sapiens

<400> 97
gcagcagtcg acattggagc agtagaagag cttagag

37

<210> 98
<211> 191
<212> PRT
<213> Homo sapiens

<400> 98

Met Val Lys Lys Leu Val Met Ala Gln Lys Arg Gly Glu Thr Arg Ala
1 5 10 15

Leu Cys Leu Gly Val Thr Met Val Val Cys Ala Val Ile Thr Tyr Tyr
20 25 30

Ile Leu Val Thr Thr Val Leu Pro Leu Tyr Gln Lys Ser Val Trp Thr
35 40 45

Gln Glu Ser Lys Cys His Leu Ile Glu Thr Asn Ile Arg Asp Gln Glu
50 55 60

Glu Leu Lys Gly Lys Lys Val Pro Gln Tyr Pro Cys Leu Trp Val Asn
65 70 75 80

Val Ser Ala Ala Gly Arg Trp Ala Val Leu Tyr His Thr Glu Asp Thr
85 90 95

Arg Asp Gln Asn Gln Gln Cys Ser Tyr Ile Pro Gly Ser Val Asp Asn
100 105 110

Tyr Gln Thr Ala Arg Ala Asp Val Glu Lys Val Arg Ala Lys Phe Gln
115 120 125

Glu Gln Gln Val Phe Tyr Cys Phe Ser Ala Pro Arg Gly Asn Glu Thr
130 135 140

-----Ser Val Leu Phe Gln Arg Leu Tyr Gly Pro Gln Ala Leu Leu Phe Ser-----

145

150

155

160

Leu Phe Trp Pro Thr Phe Leu Leu Thr Gly Gly Leu Leu Ile Ile Ala
165 170 175

Met Val Lys Ser Asn Gln Tyr Leu Ser Ile Leu Ala Ala Gln Lys
180 185 190